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TCGACCCACGCGTCCGGGAGGATCGGGAGTCGCGGGAGGATGGGCCGCGCTAGGCTCGCACTCCGGA
CGCGCCTCGC
AGTGCGCAGGGTGGGTGCCCCGCGCCTGCAGCGTCCGCCGGGGCGGCGCGGGAGGTGGCCGACAG
GCTCCGGGCC
TCGCAGCCTCAGCCCCCGGCCAGCGCGCTTTCCGACGGCGGCGCGCCGAGCCACCCGCC
CGCCCAAGGTCTCTCGCGGGCGGGAGAACGGAACCTCCCAACTTCCTGAGTTCTAAAGTTCCTGTTG
CTTCAGACAA
TGGATGAGCAATCACAAGGAATGCAAGGGCCACCTGTTCTCAGTTCCAACCACAGAAGGCCTTACGA
CCGGATATGG
GCTATAATACATTAGCCAACCTTTCGAATAGAAAAGAAAATTGGTCGCGGACAATTTAGTGAAG
TTTATAGAGCAGCCTGTCTCTTGGATGGAGTACCAGTAGCTTTAAAAAAGTGCAGATATTTGATTTA
ATGGATGCCA
AAGCACGTGCTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
TATTATGCAT
CATTCATTGAAGATAATGAACTAAACATAGTTTTTGGAACTAGCAGATGCTGGCGACCTATCCA
GAATGATCAAGCATTTTAAGAAGCAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAAGTATTTTGT
CAGCTTTGCA
GTGCATTGGAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAAACCAGCTAATGTGTTTATT
ACAGCCACTG
GGGTGGTAAAACTTGGAGATCTTGGGCTTGGCCGGTTTTTTCAGCTCAAAAACACAGCTGCAC
ATTCTTTAGTTGGTACGCCCTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACCTCAA
TCTGACATCT
GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACAAAATGAAT
TTATACTCAC
TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTTCAGATCACTATTGAGAAGAAC
TCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAGAGAAGCGACCAGACGTACCTATGTTTAT
GACGTAGCAA
AGAGGATGCATGCATGCACTGCAAGCAGCTAAACATGCAAGATCATGAAGAGTGTAACCAAAGTAATT
GAAAGTATTT
TGTGCAAAGTCGTACCTSCCCATTTATGTCTGGGTGTTAAGATTAATATTTTCAGAGCTAGTGT
GCTCTGAATCCTTAACCAGTTTTTCATATAAGCTTCATTTTGTACCAGTCACCTAAATCACCTCCTTGC
AACCCCCAAA
TGACTTTGGAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTTGAATGGCTAAAG
GTTTATAGAA
TTTCTTACAGTTTTCTGCTGATAAATTGTGTTTAGATAGACTGTCAGTGCCAAATATTGAAGG
TGCAGCTTGGCACACATCAGAATAGACTCATACCTGAGAAAAAGTATCTGAACATGTGACTTGTTTCT
TTTTTAGTAA
TTTATGGACATTGAGATGAACACAATTGTGAACTTTTGTGAAGATTTTATTTTTAAACGTTTGAAGTA
CTAGTTTTAG
TTCCTAGCAGAGTAGTTTTCAAATATGATTCTTATGATAAATGTAGACACAACTATTTGAGA
AACATTTAGAAGCTTTAGCTTATACATTCAAATGTAAGTATTAAATGTGAAGATTGGGGACAAAAT
GTGAGTCAGA
CACTGAAGAGTTTTTTGTTTTGTTTTTAATATTTTTGATATTCTCTTTCATTGAAATGGTATAAATGA
ATCCATTTAA
AAAGTGGTTAAGGATTTGTTTAGCTGGTGTGATAATAATTTTTAAAGTTGCACATTGCCCAAG
GCTTTTTTTGTGTGTTTTATTGTTGTTGTACATTTGAAAAATATTCTTTGAATAACCTTGCAGTAC
TATATTTCAA

FIGURE 1

TTTCTTTATAAATTTAAGTGCATTTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTTATT
CATAAGTTTT
ATTGAAGTTCTGATCGGTCCCCTTCAGAAATTTTTTTATATTATTCTTCAAGTTACTTTCTTA
TTTATATTGTATGTGCATTTTATCCATTAATGTTTCATACTTTCTGAGAGTATAATACCCTTTTAAAA
GATATTTGGT
ATACCAATACTTTTTCTGGATTGAAAACTTTTTTTAAACTTTTTTAAAATTTGGGCCACTCTGTATGCA
TATGTTTGGT
CTTGTTAAAGAGGAAGAAAGGATGTGTGTTATACTGTACCTGTGAATGTTGATACAGTTACAA
TTTATTTGACAAGGTTGTAATTTCTAGAATATGCTTAATAAAATGAAAACCTGGCCATGACTACAGCCAG
AACTGTTATG
AGATTAACATTTCTATTGAGAAGCTTTTGAGTAAAGTACTGTATTTGTTTCATGAAGATGACTGAGATG
GTAACACTTC
GTGTAGCTTAAGGAAATGGGCAGAATTTTCGTAAATGCTGTTGTGCAGATGTGTTTTCCCTGAA
TGCTTTTCGTATTAGTGCGCACCAGTTTCTCACAGAATTGTGAAGCCTGAAGGCCAAGAGGAAGTCACT
GTTAAAGGAC
TCTGTGCCATCTTACAACCTTGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
TCCCTTTAGC
CGATGTAAGTCTGGTTTTGTTTTTCATATGTGTTTTTCTTACACTCATTTGAATGCTTTCAA
GCATTTGTAACTTAAAAAANWAWAAAGGGCAAAAAGTCTGAACCTTGTTTTCTGAAATCTAATC
AGTTATGTAT
GGTTTCTGAAGGGTAATTTTATTTTGAATAGGTAAAGCGAAACCTGTTTTGTCWTGTTTTTCTGAG
GGCTAGATGC
ATTTTTTTTCTCACACTCTTAATGACTTTTAACATTTATACTGAGCATCCATAGATATATTCC
TAGAAGTATGAGAAGAATTATTCTTATTGACCATTAATGTATGTTTCAATTTAATGTAATATAATTGA
GATGAAATGT
TCTCTGGTTGGAACAGATACTCTCTTTTTTTTTCTTGCAATCTTTAAGAATACATAGATCTAAAATTC
ATTAGCTTGA
CCCCTCAAAGTAACTTTTAAGTAAAGATTAAAGCTTTTCTTCTCAGTGAATATATCTGCTAGA
AGGAAATAGCTGGGAAGAATTTAATGATCAGGGAAATTCATTATTTCTATATGTGGAACTTTTTGCT
TCGAATATTG
TATCTTTTTAAATCTAAATGTTTCATATTTTCTGAAGAAACCACTGTGTAAAAATCAAATTTTAATT
TTGAATGGAA
TAATTTCAAAGAACTATGAAGATGATTTGAAGCTCTAATTTATATAGTCACCTATAAAATGTT
CTTTATATGTGTTTATAAGTAAATTTTATATTGATTAAGTTAACTTTTGAATTGATTTGAGGAGCAG
TAAAATGAAA
GCTATATCTATTNCTAAACCYTATTTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAACT
TTGTTTTGTA
TGGTAAGGTTTAGGAATGGNGGATGAAGGGTATCTCTATATAAATAAAGTGCTCAACAATGTG
CAATGATTGTAAATTTAGTAAGATATTACAGCCATTTTCATGAATGCTTTACCATTCAACATAGTATCT
ATTACAAAAC
ACCTTTCTGTATCCATATACTTCAGGTGTTGCTGTTAACATTTACTATGATATTTATTTTAACCAA
ATGTTACTCA
CATTAAATGTTTATTCTTTAAAATGAATGTATTATGTTTTTAACCCACAAATGCATACTTACC
CTGTGCCTCATATTTCAATAGTACTGTAATATGGACATCTTTGTGAAATACTTTTATTTTGTATGC
TTTAAATATA
CATACAAAAGATTTCTGTTATTAGCTTTGAAAATTGTATAATATCCTAATATAAACAAAAATATAAA
AATAAAATG
AATACAGTAAAAAAAAAAAAAAAAAAAAAAAAAAGG

FIGURE 1 (cont'd)

MDEQSQGMQGPVPQFQPKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYASFIEDNELNIVLELADAGDLSRMIKHFKKQRLIPERTVWKYFVQLC
SALEHMHSRR
VMHRDIKPANVFITATGVVKLGLDLGRFFSSKTTAAHSLVGTPYYMSPERIHENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNLVSLCKKIEQCDYPPLPSDHYSEELRQLVNMCIINPDPEKRPDVTY
VYDVAKRMHA
CTASS

FIGURE 1 (cont'd)

GTCGACCCACGCGTCCGGTGGAGTATAATACTTTGTCTATTATGAGATGTCGTCTCTCGG
TGCTCTCTTTGTGCAAATTAAATTTGATGACTTGACGTTTTTTTGAAGAACTGCGGTGGAGG
AAGTTTTGGGAGTGTATATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACAT
CATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATTGTTCACAGAATATGC
TTCTCTGGGATCACTCTATGATTACATTAAACAGTAACAGAAGTGAGGAGATGGATATGGA
TCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGC
TCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGG
AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAA CATAACAACACACATGTC
CTTGGTTGGAACCTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTGTCAGA
AACTTGTGACACATATTCTATGGTGTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCC
CTTTAAAGGTTTGGAAAGGATTACAAGTAGCTTGGCTTGTAGTGGAACAAAAACGAGAGATT
AACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACATCAGTGTGGGAAGC
TGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCATCCTGGAGTCCATGTCAAA
TGACACGAGCCTTCTTGACAAGTGTAACCTATTCTACACAACAAGGCGGAGTGGAGGTG
CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGATCTCAGCTTTAAGGA
GCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAAAAGCTGACAGAGCA
GTCCAACACCCCGCTTCTCTTGCCTCTTGCTGCAAGAATGTCTGAGGAGTCTTACTTTGA
ATCTAAAACAGAGGAGTCAAACAGTGCAGAGATGTCTGTGATGATGACAGCAACAAGTAA
CGGGGAGGGCCATGGCATGAACCAAGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGA
TATCTTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
AGCCAAGCAGAATTCTTCCAAAACCATCTAAGAGAAGGGGGAAGAAAGTCAACATGGC
TCTGGGGTTTCAAGTATTTTGAATTTGTGAGAGGTGACGATGATGATGATGACGGTGA
GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAGTAATAAAATCA
CAAATGTTTGGAAAACACAAAAGTAACCTGTTTATCTCAGTCTGTACAAAAACAGTAAGG
AGGCAGAAAGCCAAGCACTGCATTTTTTAGGCCAATCACATTTACATGACCGTAATTTCTT
ATCAATTCTACTTTTTATTTTTTGCTTACAGAAAAACGGGGGGAGAATTAAGCCAAAGAAGT
ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTTGTGATCCTATATACAAT
ATAGGACTTTTAAAGTTGTGACATTCTGGCTTTTTCTTTTAAATGAATACTTTTTTAGTTTG
TATTTGACTTTATTTCTTTTATTCAAATCATTTTTTAAAACTTACATTTTGAACAAACAC
TCTTAACCTCTAATTGTTCTTTGACACGTAAGTATCTGTGACATACTTTTTTTTTCTTA
TAGCAATACACTGTAATATCAGAAATGGTTGGCCTGAGCAACCTAGTAAGACCTCGTCTC
TACTAATAATTAAAAAACTAGCTGGCATGGTAGCACACACCTGTAGTCCCAGATACTTGG
GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
GATGGCACCCTGCACTCTAGCCTGGGCAAGAGAAACAAGATCCTGTCTCAAAAAACAAAA
AAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLQFFENC GGGSFGSVYRAKMWISQDKEVAVK
KLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDM
HIMTWATDVAKGHLYLHNEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTHMS
LVGTFPMMAPEVIQSLFVSETCDTYSYGVVLMWMLTREVPFKGLEGLQVANLVVEKNERL
TIPSSCPRSPFAELLHQWEADAKRPSFKQIIISLESMSNDTSLPDKNSPLHNKAEMRC
EIEATLERLKKLERDLSFKQELKERERRLKMWEQKLTQSNTPLLLPLAARMSEESYFE
SKTEESNSAEMSCQITATSNGEHGMNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQINMQ
AKQNSSKTTSKRRGKKNMALGFSDFDLSEGGDDDDDDGEEEDNDMDNSE

CGGTGGTGGCGGCAGCGGCGGCTGCGGGGGCACCGGGCCGCGGCGCCACCATGGCCGTGC
GACAGGCGCTGGGCGCGCGGCTGCGAGCTGGGTGAGCGCTGCTGCTGCGCTTCACGGGCA
AGCCCGGCGGGCCTACGGCTTGGGGCGGCGGCGGGCCCGGCGGCGGGCTGTGTCCGCGGGG
AGCGTCCAGGCTGGGCGCGCAGGACCGGGCGCGGAGCCTCGCAGGGTGGGGCTCGGGCTTC
CTAACCGTGTCCGCTTCTTCCGCCAGTCCGGTGGCCGGGCTGGCGGCGCGGTTGCGAGCGGC
AGTTCTGTGGTGGCGGCTGGGGCTGCGCGGGCCCTTGGCGGCGGGCAGTCTTTCTGGCCT
TCGGGCTAGGGCTGGGCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGG
CCTGTGAGGAGATCCAGGCAATTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGG
ACACGAGACGCTTGCAGGGCTTTTCCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTA
AGGGCTGCAGTGTCTGTGTATGAAGCCACCATGCGCTACATTGCCCCAGAACCTGGAGG
TGACAAAGAGCACCGGGTTGCTTCCAGGGAGAGGCCAGGTACCAGTGCACCAGGAGAAG
GGCAGGAGCGAGCTCCGGGGGCCCCCTGCGCTTCCCTTGGCCATCAAGATGATGTGGAACA
TCTCGGCAGGTTCCCTCCAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAG
CGAGCCGAGTGGCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAG
GTCCCAAGCAACTAGCCCCCTCACCCCAACATCATCCGGGTTCTCCGCGCTTCACCTCTT
CCGTGCGCGCTGTGCGAGGGGCCCTGGTGGAGTACCCTGATGTGCTGCCCTCACGCTCC
ACCCTGAAGGCTGGGCCATGGCCGGACGCTGTTCCTCGTTATGAAGAACTATCCCTGTA
CCCTGCGCCAGTACCTTTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGC
TGCAGCTGTGGAAGGCGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGA
AATCCGACAACATCCTTGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGATCGCAG
ATTTTGGCTGTGCTGGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGT
ACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCTG
GCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCT
ATGAAATCTTCCGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCC
GCAGCTACCAAGAGGCTCAGTACCTGCACATGCCCGAGTCACTGCCCTGAGAGTGAAGT
AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCG
CAAATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAACTGAAGT
TAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGC
TCACAGAGAAGTGTGTGTGGAAACAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGT
GTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
CCTGCATGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTCTGTGATGGTCTG
TGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
AAGGCCTCGGGCTTGGCAAATGGAAGAACTTGAAGTGAAGTTCAGTCTGCAGTCTCTGTC
TCACAGACATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAG
TTTGGCTGTGACCTTTGCCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATG
TCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTGAGCACGTTTCAATTACGGG
AGTGGGAAATTACATGAGGCTGGGCCCTTGGCTTCCCAAGCTGTGCGTTCTGGACCAGC
TACTGAATTATTAATCTCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTGAATAT
GGGATTTAAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAATAT
TAAATGCAAAATTTACAACCTGCAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCCC

FIGURE 3

Met Ala

Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
5 10 15

Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro
20 25 30

Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala
35 40 45 50

Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
55 60 65

Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln
70 75 80

Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
85 90 95

Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys
100 105 110

Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala
115 120 125 130

Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
135 140 145

Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
150 155 160

Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu
165 170 175

Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg
180 185 190

Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly
195 200 205 210

Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala
215 220 225

FIGURE 3 (cont'd)

Gly	Ser	Ser	Ser	Glu	Ala	Ile	Leu	Asn	Thr	Met	Ser	Gln	Glu	Leu	Val	230	235	240	
Pro	Ala	Ser	Arg	Val	Ala	Leu	Ala	Gly	Glu	Tyr	Gly	Ala	Val	Thr	Tyr	245	250	255	
Arg	Lys	Ser	Lys	Arg	Gly	Pro	Lys	Gln	Leu	Ala	Pro	His	Pro	Asn	Ile	260	265	270	
Ile	Arg	Val	Leu	Arg	Ala	Phe	Thr	Ser	Ser	Val	Pro	Leu	Leu	Pro	Gly	275	280	285	290
Ala	Leu	Val	Asp	Tyr	Pro	Asp	Val	Leu	Pro	Ser	Arg	Leu	His	Pro	Glu	295	300	305	
Gly	Leu	Gly	His	Gly	Arg	Thr	Leu	Phe	Leu	Val	Met	Lys	Asn	Tyr	Pro	310	315	320	
Cys	Thr	Leu	Arg	Gln	Tyr	Leu	Cys	Val	Asn	Thr	Pro	Ser	Pro	Arg	Leu	325	330	335	
Ala	Ala	Met	Met	Leu	Leu	Gln	Leu	Leu	Glu	Gly	Val	Asp	His	Leu	Val	340	345	350	
Gln	Gln	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Ile	Leu	Val	355	360	365	370
Glu	Leu	Asp	Pro	Asp	Gly	Cys	Pro	Trp	Leu	Val	Ile	Ala	Asp	Phe	Gly	375	380	385	
Cys	Cys	Leu	Ala	Asp	Glu	Ser	Ile	Gly	Leu	Gln	Leu	Pro	Phe	Ser	Ser	390	395	400	
Trp	Tyr	Val	Asp	Arg	Gly	Gly	Asn	Gly	Cys	Leu	Met	Ala	Pro	Glu	Val	405	410	415	
Ser	Thr	Ala	Arg	Pro	Gly	Pro	Arg	Ala	Val	Ile	Asp	Tyr	Ser	Lys	Ala	420	425	430	

FIGURE 3 (cont'd)

Applicant: Acton, Susan L.
Title: NOVEL PROTEIN KINASE MOLECULES AND USES
THEREFOR
Attorney/Agent: Tracy M. Sioussat
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Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val
435 440 445 450

Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
455 460 465

Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
470 475 480

Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
485 490 495

Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
500 505 510

His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
515 520 525 530

Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
535 540 545

Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
550 555 560

Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
565 570 575

Ala Ala Leu

GTCGACCCACGCGGTCCGCCCCACGCGTTCCGGAGACATGTCTCTGTGTTTC
TCTCCCCCTCCGCTTTTGAGTCCGTTGAAGACACAATTTCTCTCTGTGCGGT
GCTTAGGAGGAGCTCCATGAACATGTATTGAATTGGACTTAGCTGAACAG
GCTGCTGGTTGGCTGCCCAGAGGGGGCAGGCTGTGTTGCTGGGAGCCTTC
CAGCTCCCTGCAGCAGTCATGGGGCAGGGTTCCCCGAGTCCGTAATCCCC
ATTTCCACCTACTTTCCCTTAGTTATTTGATTCCCTGTCTGTCTGTAATCAGC
TTAAGTGGAGCATCCCCCTTTCCTGGGAGACACGAAGCAGGAAACACTGGC
AAATATCACAGCAGTGAGTTACGACTTTGATGAGGAATTCTTCAGCCAGA
CGAGCGAGCTGGCCAAGGACTTTATTCGGAAGCTTCTGGTTAAAGAGACC
CGGAAACGGCTCACAATCCAAGAGGCTCTCAGACACCCCTGGATCACGCC
GGTGGACAACCAGCAAGCCATGGTGCAGCAGGGAGTCTGTGGTCAATCTGG
AGAACTTCAGGAAGCAGTATGTCCGCAGGCGGTGGAAGCTTTCCTTCAGC
ATCGTGTCCCTGTGCAACCACCTACCCGCTCGCTGATGAAGAAGGTGCA
CCTGAGGCCGGATGAGGACCTGAGGAACTGTGAGAGTGACACTGAGGAG
GACATCGCCAGGAGGAAAGCCCTCCACCCACGGAGGAGGAGCAGCACCT
CCTAACTGGCCTGACCTGCAGTGGCCGCCAGGGAGGTCTGGGCCCAGCGG
GGCTCCCTTCTGTGCAGACTTTTGGACCCAGCTCAGCACCAGCACCCGGGC
GTCCTGAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAAGAGCTT
GCAGGCAAGCCAGGAGACCCTGGGAGCTGTGGCTGTCTTCTGTGGAGGAG
GCTCCAGCATTCCCAAAGCTCTTAATTCTCCATAAAATGGGCTTTCCTCTG
TCTGCCATCCTCAGAGTCTGGGGTGGGAGTGTGGACTTAGGAAAACAATA
TAAAGGACATCCTCATCATCACGGGGTGAAGGTCAGACTAAGGCAGCCTT
CTTCACAGGCTGAGGGGGTTTTCAGAACCAGCCTGGCCAAAAAATTACACCAG
AGAGACAGAGTCCTCCCCATTGGGAACAGGGTGATTGAGGAAAGTGAACC
TTGGGTGTGAGGGACCAATCCTGTGACCTCCCAGAACCATGGAAGCCAGG
ACGTCAGGCTGACCAACACCTCAGACCTTCTGAAGCAGCCCATTGCTGGC
CCGCCATGTTGTAATTTTGCTCATTTTTATTAACTTCTGGTTTACCTGATG
CTTGGCTTCTTTTAGGGCTACCCCCATCTCATTTCCTTTAGCCCGTGTGCCT
GTA ACTCTGAGGGGGGGCACCAGTGGGGTGTGAGTGGGCAGAATCTCA
GAAGGTCCTCCTGAACCGTCCGCGCAGGCCTGCAGTGGGCCTGCCTCCTC
CTTGCTTCCCTAACAGGAAGGTGTCCAGTTCAAGAGAACCCACCCAGAGA
CTGGGAGTGGTGGCTCACGCCTATAATCCCTGCGCTTTGGCAGTCCGAGG
CAGGGGAATTGCTTGA ACTCAGGAGTTGGAGACCAGCCTGGGCAACATGG
CAAAACGCAGTCTGTACAAAAAATACAAAAAATTAGCCAGGTGTAGGGGT
AGGCACCTGGCATCCCAGCTACTCCAGGGGCTGAGGTGACAGCATTGCTT
AAGCCCAGAAGGTGAGGCTGCAGTGAGCTGAGATCACGCCACTGCACTC
CAGTCTGGGTGACAGAGAGAGACCATATCCAAAAAAGGG
CGGCCGC

LFDSL SVVLSLSGAS PFLGDTKQETLANITAVSYDFDEEFFSQTSELAKDFIRKL
LVKETRKRLTIQEALRHPWITPVDNQAMVRRESVVNLENFRKQYVRRRWK
LSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKALHPRRSSTS

FIGURE 4

Applicant: Acton, Susan L.

Title: NOVEL PROTEIN KINASE MOLECULES AND USES THEREFOR

Attorney/Agent: Tracy M. Sioussat

Docket No.: MPI1998-052PIRDV10DV1M

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T A L A K E L R E L R I E E T N R P M 19
G A G C A T T A G C C A A G A A C T A A G A A C T C C G A T T G A A G A A A C C C C A A T G 57
K K V T D Y S S S S B E S E S S E E E E 39
A A G A A G G T G A C T G A T T A C T C C T C C A G T G A G G A G T C A G A A A G T A C G A G G A G G A G 117
E D G E S E T H D G T V A V S D I P R L 59
G A A G A T G A G A G C G A G A C C A T G A T C G G A C A G T G C T G T C A G C A T A C C A G A C T G 177
I P T G A P G S N E Q Y N V G H V G T H 79
A T A C C A C A G G A G C T C C A G C A G A A C G A G C A G T A C A A T G T G C G A A T G G T G G G A C C A T 237
G L E T S H A D S F S G S I S R E O T L 99
O G G C T G G A G A C C T C T C A T G C G G A C A G T T T C A G C G C A G T A T T C A A G A G A A C C T T G 297
M I R E T S G E K K R S G H S D S N G F 119
A T G A T T A G A G A G A C G T C T G A G A A G A A G C A T T C T G C C A C A G T G A C A C C A A T G C C T T T 357
A G H I N L P D L V Q Q S H S P A G T P 139
G C T G C C A C A T C A A C C T C C T G C T G G T G C A G C A G A C C A T T C T C C A G C T G A A C C C G 417
T E G L G R V S T H S Q E M D S G T E Y 159
A C T G A G G A C T G G G C G C G T C T C A A C C A T T C C C A G G A G A T G G A C T C T G G G A C T G A A T A T 477
G A G S S T K A S F T P F V D P R V Y Q 179
G C C A T G G G A G C A C C A C C A A G C C T T C A C C C C T T T G T G G A C C C C A G A G T A T A C C A G 537
T S P T D E D E D E S S A A A L F T 199
A G T T C T C C C A C T G A T G A A G A G G A T G A G G A A T C A T C A G C C A G C C T C T G T T T A C T 597
S E L L R Q E Q A K L N E A R K I S V V 219
A G C G A A C T T C T T A G G C A A G A A C A G C A A C C A A G A A G A A T T T G G T G T A 657
N V N P T N I R P H S D T P E I R K Y K 239
A A T G T A A A C C A C C A A C A T T C C G C C T C A T A C C G A C A C A C A G A A A T C A G A A A A T A C A A G 717
K R F N S E I L C A A L W G V N L L V G 259
A A A C A T T C A C T C A G A A A T A C T T G T G C A G C T G T G G G T G T A A A C C T T C T G G T G G G 777
T E N G L M L L D R S G Q G K V Y N L I 279
A C T G A A A A T G C C T G A T G C T T T G G A C C A G A G T G G C A A G C C A A G T C T A A T C T G A T C 837
N R R R F Q Q M D V L E G L N V L V T I 299
A A C C G G A G C A T T T C A G C A G A T G G A T G T G C T A G A G G A C T G A A T G T C C T T G T G A C A A T 897
S G K K N K L R V Y Y L S W L R N R I L 319
T C A G A A A G A A T A A G C T A C G A G T T T A C T A T C T T T C A T G G T T A A G A A C A G A A T A C T A 957
H N D P E V E K K Q G W I T V G D L E G 339
C A T A A T G A C C A G A A G T A G A A A G A A A C A A G C C T G A T C A C T G T T G G G A C T T G A A G C 1017
C I H Y K V V K Y E R I K F L V I A L K 359
T G T A T A C A T A T A A G T T A A T A T G A A A G A T C A A A T T T T T G G T G A T T G C C T T A A A G 1077
N A V E I Y A W A P K P Y H K F M A F K 379
A A T C C T G T G A A A T A T G C T T G G C C T C T A A A C C G T A T C A T A A A T T C A T G C A T T T A A G 1137
S F A D L Q H K P L L V D L T V E E G Q 399
T C T T T G C A G A T C T C C A G C A C A A G C C T C T A G T T G A T C T C A C G G T A G A A G A A G G T C A A 1197
R L K V I P G S H T G F H V I D V D S G 419

FIGURE 5

AGA TTA AAG GTT ATT TTT GGT TCA CAC ACT GGT TTC CAT GTA ATT GAT GTT GAT TCA GGA 1257
N S Y D I Y I P S H I Q G N I T P H A I 439
AAC TCT TAT GAT ATC TAC ATA CCA TCT CAT ATT CAG GGC AAT ATC ACT OCT CAT GCT ATT 1317
V I L P K
GTC ATC TTG CCT AAA 444
1332

FIGURE 5 (cont'd)